SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (I) APPLICANT: NAKAMURA, SEIJI SAKURAI, TAKASHI NEZU, JUNI-ICHI
- (ii) TITLE OF INVENTION: GENE ENCODING ADSEVERIN
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
 - (B) STREET: P.O. Box 747
 - (C) CITY: Falls Church
 - (D) STATE: VA
 - (E) COUNTRY: USA
 - (F) ZIP: 22040-0747
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: MURPHY Jr., Gerald M.
 - (B) REGISTRATION NUMBER: 28,977
 - (C) REFERENCE/DOCKET NUMBER: 230-110P
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703) 205-8000
 - (B) TELEFAX: (703) 205-8050
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Lys Val Ala His Val Lys Gln Ile Pro Phe Asp Ala

- (2) INFORMATION FOR SEQ ID NO:2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 - Val Leu Thr Asn Asp Leu Thr Ala Gln 1
- (2) INFORMATION FOR SEQ ID NO:3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - . (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
 - Ile Thr Asn Arg Lys
 1 5
- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2418 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 27...2171
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
- CGGCCGGAAC ATCGCGTGCC CGAGTC ATG GCC CAG GGG CTG TAC CAC GAG GAG

 Met Ala Gln Gly Leu Tyr His Glu Glu

 1
- TTC GCC CGC GCG GGC AAG CGG GCG GGG CTG CAG GTC TGG AGA ATT GAG 101

Phe 10	Ala	Arg	Ala	Gly	Lys 15	Arg	Ala	Gly	Leu	Gln 20	Val	Trp	Arg	Ile	Glu 25	
AAG Lys	CTG Leu	GAG Glu	CTG Leu	GTG Val 30	CCG Pro	GTG Val	CCC Pro	GAG Glu	AGC Ser 35	GCG Ala	TAT Tyr	GGC Gly	AAC Asn	TTC Phe 40	TAC Tyr	149
GTC Val	GGG Gly	GAT Asp	GCC Ala 45	TAC Tyr	CTG Leu	GTG Val	CTC Leu	CAC His 50	ACG Thr	ACG Thr	CAG Gln	GCC Ala	AGC Ser 55	CGG Arg	GGC Gly	197
TTC Phe	ACC Thr	TAC Tyr 60	CGC Arg	CTG Leu	CAC His	TTC Phe	TGG Trp 65	CTG Leu	GGA Gly	AAG Lys	GAG Glu	TGT Cys 70	ACT Thr	CAG Gln	GAT Asp	245
GAA Glu	AGC Ser 75	ACA Thr	GCA Ala	GCT Ala	GCC Ala	ATC Ile 80	TTT Phe	ACT Thr	GTT Val	CAG Gln	ATG Met 85	GAT Asp	GAC Asp	TAT Tyr	TTG Leu	293
GGT Gly 90	GGC Gly	AAA Lys	CCT Pro	GTG Val	CAG Gln 95	AAC Asn	AGA Arg	GAA Glu	CTT Leu	CAA Gln 100	GGC Gly	TAT Tyr	GAG Glu	TCT Ser	ACG Thr 105	341
GAT Asp	TTT Phe	GTT Val	GGC Gly	TAC Tyr 110	TTT Phe	AAA Lys	GGA Gly	GGT Gly	CTG Leu 115	AAA Lys	TAC Tyr	AAG Lys	GCT Ala	GGC Gly 120	GGT Gly	389
GTG Val	GCG Ala	TCT :Ser	GGA Gly 125	CTC Leu	AAT Asn	CAT His	GTG Val	CTT Leu 130	ACA Thr	AAT Asn	GAC Asp	TTG Leu	ACT Thr 135	GCT Ala	CAG Gln	437
AGG Arg	CTC Leu	CTG Leu 140	CAT His	GTG Val	AAA Lys	GGT Gly	CGG Arg 145	AGA Arg	GTC Val	GTC Val	AGG Arg	GCC Ala 150	ACG Thr	GAA Glu	GTT Val	485
CCC Pro	CTA Leu 155	Ser	TGG Trp	GAC Asp	AGT Ser	TTC Phe 160	AAC Asn	AAG Lys	GGT Gly	GAC Asp	TGC Cys 165	TTC Phe	ATC Ile	ATT Ile	GAC Asp	533
Leu	Gly	Thr	Glu	Ile	Tyr	CAG Gln	Trp	Cys	Gly	Ser	Ser	TGC Cys	AAC Asn	AAG Lys	TAC Tyr 185	581
GAG Glu	CGC Arg	CTG Leu	AAG Lys	GCC Ala 190	AGC Ser	CAG Gln	GTT Val	GCC Ala	ATC Ile 195	GGC Gly	ATT Ile	CGG Arg	GAC Asp	AAT Asn 200	GAA Glu	629
AGG Arg	AAA Lys	GGC Gly	AGA Arg 205	GCT Ala	CAĠ Gln	CTG Leu	ATT Ile	GTG Val 210	GTA Val	GAA Glu	GAA Glu	GGG Gly	AGT Ser 215	GAA Glu	CCA Pro	677
TCA Ser	GAG Glu	CTT Leu 220	Thr	AAG Lys	GTA Val	TTA Leu	GGG Gly 225	GAA Glu	AAG Lys	CCA Pro	AAG Lys	CTT Leu 230	AGG Arg	GAT Asp	GGA Gly	725
GAA Glu	GAT Asp 235	Asp	GAT Asp	GAC Asp	ATC Ile	AAA Lys 240	GCA Ala	GAT Asp	ATA Ile	ACT	AAT Asn 245	AGG Arg	AAA Lys	ATG Met	GCT Ala	773
AAA Lys	CTC Leu	TAC Tyr	ATG Met	GTT Val	TCA Ser	GAT Asp	GCC Ala	AGT Ser	GGC Gly	TCC Ser	ATG Met	AAA Lys	GTG Val	AGT Ser	CTG Leu	821

250	255	260	265
	Pro Phe Ser Met A	GCG ATG CTT CTG TCT C Ala Met Leu Leu Ser C 275	
		AAA CAG ATT TTT GTA T Lys Gln Ile Phe Val T 295	
		AAG GCT GCC ATG AAG A Lys Ala Ala Met Lys T 310	
		TCT ACG AAT ACC CAA A Ser Thr Asn Thr Gln I 325	
GTT CTT CCA GAA GGA Val Leu Pro Glu Gly 330	GGT GAA ACA CCA A Gly Glu Thr Pro 1 335	ATC TTC AAA CAG TTC T Lle Phe Lys Gln Phe P 340	TT AAG 1061 he Lys 345
GAC TGG AGA GAT AGA Asp Trp Arg Asp Arg 350	Asp Gln Ser Asp C	GGC TTC GGG AAA GTG T Gly Phe Gly Lys Val T B55	AT GTC 1109 yr Val 60
		ATT CCA TTT GAT GCC T lle Pro Phe Asp Ala S 375	
		CAG CAT CAC GTG GTG G Gln His His Val Val A 390	
		GTA GAA AAC AAC GGT A Val Glu Asn Asn Gly A 405	
		TTC TAT GGT GGT GAT T Phe Tyr Gly Gly Asp C 420	
	Tyr Pro Arg Gly G	CAG ATT ATC TAC ACC T Sin Ile Ile Tyr Thr T 135 4	
		ACA ACC TCC GCA TTC C Thr Thr Ser Ala Phe L 455	
		CAG GCT GTG CAG ATT C Sin Ala Val Gin Ile A 470	
		CTG AGT TTG TTC AAA G Leu Ser Leu Phe Lys A 485	
		CCA AAG AAA GAA GGT C Ger Lys Lys Glu Gly G 500	

CCA GCC C	CCC CCT Pro Pro	ATA C Ile A 510	GC CTC arg Leu	TTT Phe	CAA Gln	GTC Val 515	CGA Arg	AGA Arg	AAC Asn	CTG Leu	GCT Ala 520	TCG Ser	1589
ATC ACC A	AGA ATT Arg Ile 525	ATG G Met G	SAG GTA Slu Val	GAT Asp	GTT Val 530	GAT Asp	GCA Ala	AAC Asn	TCA Ser	TTG Leu 535	AAT Asn	TCC Ser	1637
AAT GAT G Asn Asp V	GTT TTT Val Phe 540	GTC C	CTG AAA Leu Lys	CTG Leu 545	CGA Arg	CAA Gln	AAT Asn	AAT Asn	GGC Gly 550	TAC Tyr	ATC Ile	TGG Trp	1685
ATA GGA A Ile Gly I 555	AAA GGC Lys Gly	TCC A Ser T	ACA CAG Thr Gln 560	GAG Glu	GAG Glu	GAG Glu	AAA Lys	GGA Gly 565	GCA Ala	GAG Glu	TAC Tyr	GTG Val	1733
GCA AGC G Ala Ser V 570	STC CTC Val Leu	Lys C	GC AAA Cys Lys 575	ACT Thr	TCG Ser	ACG Thr	ATT Ile 580	CAG Gln	GAA Glu	GGC Gly	AAG Lys	GAA Glu 585	1781
CCA GAG (GAG TTT Glu Phe	TGG A Trp A 590	AAT TCC Asn Ser	CTT Leu	GGA Gly	GGG Gly 595	AAA Lys	AAA Lys	GAC Asp	TAC Tyr	CAG Gln 600	ACC Thr	1829
TCT CCT (CTG CTA Leu Leu 605	GAA T Glu S	CC CAG Ser Gln	GCT Ala	GAA Glu 610	GAC Asp	CAT His	CCA Prò	CCT Pro	CGG Arg 615	CTT Leu	TAC Tyr	1877
GGC TGC TGL	TCC AAC Ser Asn 620	AAA A Lys T	ACT GGA Thr Gly	AGA Arg 625	TTC Phe	ATT Ile	ATT	GAA Glu	GAG Glu 630	GTT Val	CCA Pro	GGA Gly	1925
GAG TTC A	ACC CAG Thr Gln	GAT G	GAT TTA Asp Leu 640	GCA Ala	GAA Glu	GAT Asp	GAT Asp	GTC Val 645	ATG Met	CTG Leu	TTA Leu	GAT Asp	1973
GCT TGG (Ala Trp (650	GAA CAG Glu Gln	Ile F	ITT ATT Phe Ile 655	TGG Trp	ATT Ile	GGA Gly	AAA Lys 660	GAT Asp	GCC Ala	AAT Asn	GAA Glu	GTT Val 665	2021
GAG AAA G	TCA GAA Ser Glu	TCT C Ser I 670	CTG AAG Leu Lys	TCT Ser	GCC Ala	AAA Lys 675	ATA Ile	TAC Tyr	CTT Leu	GAG Glu	ACC Thr 680	GAC Asp	2069
CCT TCT (GGA AGA Gly Arg 685	GAC A	AAG AGG Lys Arg	ACG Thr	CCA Pro 690	ATT Ile	GTC Val	ATC Ile	ATA Ile	AAA Lys 695	CAG Gln	GGT Gly	2117
CAT GAG	CCA CCT Pro Pro 700	ACT Thr E	ITC ACA Phe Thr	GGC Gly 705	TGG Trp	TTC Phe	CTG Leu	GGC Gly	TGG Trp 710	GAT Asp	TCC Ser	AGC Ser	2165
AGG TGG ' Arg Trp 715	TAAACTG.	ATT TI	ITGTAGG	AA A)AAAA	CAAA'	r ati	AATG(GGC	AGC'	rgtc(CCA	2221
GGGGGAA	GG AGGA	GCTTGT	TTAAC	TTTA	G AA	AATT	AACC	TCA	GCCA'	TAT (GGCT	ATTTTT	2281
CCGTGCTT	AG AATT	GGTTTC	G AAATI	TCTT	TAI	AACT	GGAA	TTT	CTT	ATG '	TAA'	TATTTT	2341

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 715 amino acids
 - (B) TYPE: amino acid ·
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Gln Gly Leu Tyr His Glu Glu Phe Ala Arg Ala Gly Lys Arg

Ala Gly Leu Gln Val Trp Arg Ile Glu Lys Leu Glu Leu Val Pro Val 20 25 30

Pro Glu Ser Ala Tyr Gly Asn Phe Tyr Val Gly Asp Ala Tyr Leu Val 35 40 45

Leu His Thr Thr Gln Ala Ser Arg Gly Phe Thr Tyr Arg Leu His Phe 50 60

Trp Leu Gly Lys Glu Cys Thr Gln Asp Glu Ser Thr Ala Ala Ala Ile 65 70 75 80

Phe Thr Val Gln Met Asp Asp Tyr Leu Gly Gly Lys Pro Val Gln Asn 85 90 95

Arg Glu Leu Gln Gly Tyr Glu Ser Thr Asp Phe Val Gly Tyr Phe Lys
100 105 110

Gly Gly Leu Lys Tyr Lys Ala Gly Gly Val Ala Ser Gly Leu Asn His 115 120 125

Val Leu Thr Asn Asp Leu Thr Ala Gln Arg Leu Leu His Val Lys Gly 130 135 140

Arg Arg Val Val Arg Ala Thr Glu Val Pro Leu Ser Trp Asp Ser Phe 145 150 155 160

Asn Lys Gly Asp Cys Phe Ile Ile Asp Leu Gly Thr Glu Ile Tyr Gln 165 170 175

Trp Cys Gly Ser Ser Cys Asn Lys Tyr Glu Arg Leu Lys Ala Ser Gln 180 185 190

Val Ala Ile Gly Ile Arg Asp Asn Glu Arg Lys Gly Arg Ala Gln Leu 195 200 205

Ile Val Val Glu Glu Gly Ser Glu Pro Ser Glu Leu Thr Lys Val Leu 210 215 220

Gly Glu Lys Pro Lys Leu Arg Asp Gly Glu Asp Asp Asp Ile Lys 225 230 235 240 Ala Asp Ile Thr Asn Arg Lys Met Ala Lys Leu Tyr Met Val Ser Asp 245 Ala Ser Gly Ser Met Lys Val Ser Leu Val Ala Glu Glu Asn Pro Phe 260 Ser Met Ala Met Leu Leu Ser Glu Glu Cys Phe Ile Leu Asp His Gly 280 Ala Ala Lys Gln Ile Phe Val Trp Lys Gly Lys Asp Ala Asn Pro Gln 295 Glu Arg Lys Ala Ala Met Lys Thr Ala Glu Glu Phe Leu Gln Gln Met . 315 Asn Tyr Ser Thr Asn Thr Gln Ile Gln Val Leu Pro Glu Gly Gly Glu 330 Thr Pro Ile Phe Lys Gln Phe Phe Lys Asp Trp Arg Asp Arg Asp Gln Ser Asp Gly Phe Gly Lys Val Tyr Val Thr Glu Lys Val Ala His Val 360 Lys Gln Ile Pro Phe Asp Ala Ser Lys Leu His Ser Ser Pro Gln Met 375 Ala Ala Gln His His Val Val Asp Asp Gly Ser Gly Lys Val Gln Ile 395 390 Trp Arg Val Glu Asn Asn Gly Arg Val Glu Ile Asp Arg Asn Ser Tyr 410 Gly Glu Phe Tyr Gly Gly Asp Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro 425 Arg Gly Gln Ile Ile Tyr Thr Trp Gln Gly Ala Asn Ala Thr Arg Asp 440 Glu Leu Thr Thr Ser Ala Phe Leu Thr Val Gln Leu Asp Arg Ser Leu 460 Gly Gly Gln Ala Val Gln Ile Arg Val Ser Gln Gly Lys Glu Pro Ala 475 470 His Leu Leu Ser Leu Phe Lys Asp Lys Pro Leu Ile Ile Tyr Lys Asn 490 Gly Thr Ser Lys Lys Glu Gly Gln Ala Pro Ala Pro Pro Ile Arg Leu 505 500 Phe Gln Val Arg Arg Asn Leu Ala Ser Ile Thr Arg Ile Met Glu Val 520 Asp Val Asp Ala Asn Ser Leu Asn Ser Asn Asp Val Phe Val Leu Lys 535 Leu Arg Gln Asn Asn Gly Tyr Ile Trp Ile Gly Lys Gly Ser Thr Gln 550 Glu Glu Glu Lys Gly Ala Glu Tyr Val Ala Ser Val Leu Lys Cys Lys

Thr Ser Thr Ile Gln Glu Gly Lys Glu Pro Glu Glu Phe Trp Asn Ser 585 580 Leu Gly Gly Lys Lys Asp Tyr Gln Thr Ser Pro Leu Leu Glu Ser Gln 600 Ala Glu Asp His Pro Pro Arg Leu Tyr Gly Cys Ser Asn Lys Thr Gly 615 . Arg Phe Ile Ile Glu Glu Val Pro Gly Glu Phe Thr Gln Asp Asp Leu Ala Glu Asp Asp Val Met Leu Leu Asp Ala Trp Glu Gln Ile Phe Ile 645 Trp Ile Gly Lys Asp Ala Asn Glu Val Glu Lys Ser Glu Ser Leu Lys 665 Ser Ala Lys Ile Tyr Leu Glu Thr Asp Pro Ser Gly Arg Asp Lys Arg 680 Thr Pro Ile Val Ile Ile Lys Gln Gly His Glu Pro Pro Thr Phe Thr 695

(2) INFORMATION FOR SEQ ID NO:6:

- . (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2630 base pairs

Gly Trp Phe Leu Gly Trp Asp Ser Ser Arg Trp 710

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 79..2223
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGGTTCCTC CTGCTGCTCT CGGTTTAGTC CAAGATCAGC GATATCACGC GTCCCCCGGA															60		
GCAT	rcgco	GTG (CAGG	AGCC					CTA Leu 5								111
CGG Arg	GCG Ala	GGC Gly	AAG Lys 15	CAG Gln	GCG Ala	GGG Gly	CTG Leu	CAG Gln 20	GTC Val	TGG Trp	AGG Arg	ATT Ile	GAG Glu 25	AAG Lys	CTG Leu		159
GAG Glu	CTG Leu	GTG Val 30	CCC Pro	GTG Val	CCC Pro	CAG Gln	AGC Ser 35	GCT Ala	CAC His	GGC Gly	GAC Asp	TTC Phe 40	TAC Tyr	GTC Val	GGG Gly		207

GAT Asp	GCC Ala 45	TAC Tyr	CTG Leu	GTG Val	CTG Leu	CAC His 50	ACG Thr	GCC Ala	AAG Lys	ACG Thr	AGC Ser 55	CGA Arg	GGC Gly	TTC Phe	ACC Thr	255
TAC Tyr 60	CAC His	CTG Leu	CAC His	TTC Phe	TGG Trp 65	CTC Leu	GGA Gly	AAG Lys	GAG Glu	TGT Cys 70	TCC Ser	CAG Gln	GAT Asp	GAA Glu	AGC Ser 75	303
ACA Thr	GCT Ala	GCT Ala	GCC Ala	ATC Ile 80	TTC Phe	ACT Thr	GTT Val	CAG Gln	ATG Met 85	GAT Asp	GAC Asp	TAT Tyr	TTG Leu	GGT Gly 90	GGC Gly	351
AAG Lys	CCA Pro	GTG Val	CAG Gln 95	AAT Asn	AGA Arg	GAA Glu	CTT Leu	CAA Gln 100	GGA Gly	TAT Tyr	GAG Glu	TCT Ser	AAT Asn 105	GAC Asp	TTT Phe	399
GTT Val	AGC Ser	TAT Tyr 110	TTC Phe	AAA Lys	GGC Gly	GGT Gly	CTG Leu 115	AAA Lys	TAC Tyr	AAG Lys	GCT Ala	GGA Gly 120	GGC Gly	GTG Val	GCA Ala	447
TCT Ser	GGA Gly 125	TTA Leu	AAT Asn	CAT His	GTT Val	CTT Leu 130	ACG Thr	AAC Asn	GAC Asp	CTG Leu	ACA Thr 135	GCC Ala	AAG Lys	AGG Arg	CTC Leu	495
CTA Leu 140	CAT His	GTG Val	AAG Lys	GGT Gly	CGT Arg 145	AGA Arg	GTG Val	GTG Val	AGA Arg	GCC Ala 150	ACA Thr	GAA Glu	GTT Val	CCC Pro	CTT Leu 155	543
AGC Ser	TGG Trp	GAC Asp	AGT Ser	TTC Phe 160	AAC Asn	AAG Lys	GGT Gly	GAC Asp	TGC Cys 165	TTC Phe	ATC Ile	ATT Ile	GAC Asp	CTT Leu 170	GGC Gly	591
ACC Thr	GAA Glu	ATT Ile	TAT Tyr 175	CAG Gln	TGG Trp	TGT Cys	GGT Gly	TCC Ser 180	TCG Ser	TGC Cys	AAC Asn	AAA Lys	тат Туг 185	GAA Glu	CGT Arg	639
CTG Leu	AAG Lys	GCA Ala 190	Asn	CAG Gln	GTA Val	GCT Ala	ACT Thr 195	GGC Gly	ATT Ile	CGG Arg	TAC Tyr	AAT Asn 200	GAA Glu	AGG Arg	AAA Lys	687
GGA Gly	AGG Arg 205	Ser	GAA Glu	CTA Leu	ATT Ile	GTC Val 210	GTG Val	GAA Glu	GAA Glu	GGA Gly	AGT Ser 215	GIu	CCC Pro	TCA Ser	GAA Glu	735
CTT Leu 220	Ile	AAG Lys	GTC Val	TTA Leu	GGG Gly 225	GAA Glu	AAG Lys	CCA Pro	GAG Glu	CTT Leu 230	CCA Pro	GAT Asp	GGA Gly	GGT Gly	GAT Asp 235	783
GAT Asp	GAT Asp	GAC Asp	ATT	ATA Ile 240	Ala	GAC Asp	ATA Ile	AGT Ser	AAC Asn 245	Arg	AAA Lys	ATG Met	GCT Ala	AAA Lys 250	Leu	831
TAC Tyr	ATG Met	GTT Val	TCA Ser 255	Asp	GCA Ala	AGT Ser	GGC Gly	TCC Ser 260	Met	AGA Arg	GTG Val	ACT Thr	GTG Val 265	GTG Val	GCA Ala	879
GAA Glu	GAA Glu	AAC Asn 270	CCC Pro	TTC Phe	TCA Ser	ATG Met	GCA Ala 275	Met	CTG Leu	CTG Leu	TCT Ser	GAA Glu 280	Glu	TGC Cys	TTT Phe	927

ATT Ile	TTG Leu	GAC Asp	CAC His	GGG Gly	GCT Ala	Ala	AAA Lys	CAA Gln	ATT Ile	TTC Phe	GTA Val 295	TGG Trp	AAA Lys	GGT Gly	AAA Lys	975
Asp	285 GCT Ala	AAT Asn	CCC Pro	CAA Gln	GAG Glu 305	290 AGG Arg	AAG Lys	GCT Ala	GCA Ala	ATG Met 310	AAG	ACA Thr	GCT Ala	GAA Glu	GAA Glu 315	1023
300 TTT Phe	CTA Leu	CAG Gĺn	CAA Gln	ATG Met 320	ААТ	TAT Tyr	TCC Ser	AAG Lys	AAT Asn 325	ÄCC	CAA Gln	ATT Ile	CAA Gln	GTT Val 330	CTT Leu	1071
CCA Pro	GAA Glu	GGA Gly	GGT Gly 335	GAA Glu	ACA Thr	CCA Pro	ATC Ile	TTC Phe 340	AAA Lys	CAG Gln	TTT Phe	TTT Phe	AAG Lys 345	GAC Asp	TGG Trp	1119
AGA Arg	GAT Asp	AAA Lys 350	GAT Asp	CAG Gln	AGT Ser	GAT Asp	GGC Gly 355	TTC Phe	GGG Gly	AAA Lys	GTT Val	TAT Tyr 360	GTC Val	ACA Thr	GAG Glu	1167
AAA Lys	GTG Val 365	GCT Ala	CAA Gln	ATA Ile	AAA Lys	CAA Gln 370	ATT Ile	CCC Pro	TTT Phe	GAT Asp	GCC Ala 375	TCA Ser	AAA Lys	TTA Leu	CAC His	1215
AGT Ser 380	TCT Ser	CCG Pro	CAG Gln	ATG Met	GCA Ala 385	GCC Ala	CAG Gln	CAC His	AAT Asn	ATG Met 390	GTG Val	GAT Asp	GAT Asp	GGT Gly	TCT Ser 395	1263
GGC Gly	AAA Lys	GTG Val	GAG Glu	ATT Ile 400	TGG Trp	CGT Arg	GTA Val	GAA Glu	AAC Asn 405	AÀT Asn	GGT Gly	AGG Arg	ATC Ile	CAA Gln 410	GTT Val	1311
GAC Asp	CAA Gln	AAC Asn	TCA Ser 415	TAT Tyr	GGT Gly	GAA Glu	TTC Phe	TAT Tyr 420	GGT Gly	GGT Gly	GAC Asp	TGC Cys	TAC Tyr 425	ATC Ile	ATA Ile	1359.
CTC Leu	TAC Tyr	ACC Thr 430	Tyr	CCC Pro	AGA Arg	GGA Gly	CAG Gln 435	Ile	ATC Ile	TAC Tyr	ACG Thr	TGG Trp 440	CAA Gln	GGA Gly	GCA Ala	1407
AAT Asn	GCC Ala 445	ACA Thr	CGA Arg	GAT Asp	GAG Glu	CTG Leu 450	ACA Thr	ACA Thr	TCT Ser	GCG Ala	TTC Phe 455	Leu	ACT Thr	GTT Val	CAG Gln	1455
TTG Leu 460	GAT Asp	CGG Arg	TCC Ser	CTT Leu	GGA Gly 465	Gly	CAG Gln	GCT Ala	GTG Val	CAG Gln 470	ATC Ile	CGA Arg	GTC Val	TCC Ser	CAA Gln 475	1503
GGC Gly	AAA Lys	GAG Glu	CCT Pro	GTT Val 480	His	CTA Leu	CTG Leu	AGT Ser	TTG Leu 485	TTC	AAA Lys	GAC Asp	AAA Lys	CCG Pro 490	CTC Leu	1551
ATT Ile	ATT Ile	TAC Tyr	AAG Lys 495	Asn	GGA Gly	ACA Thr	TCA Ser	AAG Lys 500	AAA Lys	GGA Gly	GGT Gly	CAG Gln	GCA Ala 505	CCT Pro	GCT Ala	1599
CCC Pro	CCT Pro	ACA Thr 510	Arg	CTC Leu	TTT Phe	CAA Gln	GTC Val 515	Arg	AGA Arg	AAC Asn	CTG Leu	GCA Ala 520	Ser	ATC Ile	ACC Thr	1647
AGA	ATT	GTG	GAG	GTT	GAT	GTT	GAT	GCA	TAA	TCA	CTG	TAA	TCT	AAC	GAT	1695

Arg	Ile 525	Val	Glu	Val	Asp	Val 530	Asp	Ala	Asn	Ser	Leu 535	Asn	Ser	Asn	Asp	
GTT Val 540	TGT Cys	GTC Val	CTG Leu	AAA Lys	CTG Leu 545	CCA Pro	CAA Gln	AAT Asn	AGT Ser	GGC Gly 550	TAC Tyr	ATC Ile	TGG Trp	GTA Val	GGA Gly 555	1743
AAA Lys	GGT Gly	GCT Ala	AGC Ser	CAG Gln 560	GAG Glu	GAG Glu	Glu	AAA Lys	Gly.	GCA Ala	GAG Glu	TAT Tyr	GTA Val	GCA Ala 570	Ser	1791
GTC Val	CTA Leu	AAG Lys	TGC Cys 575	AAA Lys	ACC Thr	TTA Leu	AGG Arg	ATC Ile 580	CAA Gln	GAA Glu	GGC Gly	GAG Glu	GAG Glu 585	CCA Pro	GAG Glu	1839
GAG Glu	TTC Phe	TGG Trp 590	AAT Asn	TCC Ser	CTT Leu	GGA Gly	GGG Gly 595	AAA Lys	AAA Lys	GAC Asp	TAC Tyr	CAG Gln 600	ACC Thr	TCA Ser	CCA Pro	1887
CTA Leu	CTG Leu 605	GAA Glu	ACC Thr	CAG Gln	GCT Ala	GAA Glu 610	GAC Asp	CAT His	CCA Pro	CCT Pro	CGG Arg 615	CTT Leu	TAC Tyr	GGC Gly	TGC Cys	1935
TCT Ser 620	AAC Asn	AAA Lys	ACT Thr	GGA Gly	AGA Arg 625	Phe	GTT Val	ATT Ile	GAA Glu	GAG Glu 630	ATT Ile	CCA Pro	GGA Gly	GAG Glu	TTC Phe 635	1983
ACC Thr	CAG Gln	GAT Asp	GAT Asp	TTA Leu 640	GCT Ala	GAA Glu	GAT Asp	GAT Asp	GTC Val 645	ATG Met	TTA Leu	CTA Leu	GAT Asp	GCT Ala 650	TGG Trp	2031
GAA Glu	CAG Gln	ATA Ile	TTT Phe 655	ATT Ile	TGG Trp	ATT Ile	GGC Gly	AAA Lys 660	GAT Asp	GCT Ala	AAT Asn	GAA Glu	GTT Val 665	GAG Glu	AAA Lys	2079
AAA Lys	GAA Glu	TCT Ser 670	CTG Leu	AAG Lys	TCT Ser	GCC Ala	AAA Lys 675	ATG Met	TAC Tyr	CTT Leu	GAG Glu	ACA Thr 680	GAC Asp	CCT Pro	TCT Ser	2127
GGA Gly	AGA Arg 685	GAC Asp	AAG Lys	AGG Arg	ACA Thr	CCA Pro 690	ATT Ile	GTC Val	ATC Ile	Ile	AAA Lys 695	Gln	GGC Gly	CAT His	GAG Glu	2175
CCA Pro 700	Pro	ACA Thr	TTC Phe	ACA Thr	GGC Gly 705	TGG Trp	TTC Phe	CTG Leu	GGC Gly	TGG Trp 710	GAT Asp	TCC Ser	AGC Ser	AAG Lys	TGG Trp 715	2223
TAA	ATTG	GTA	TTTG	TAAA	AA G	CAAA	CAAA	C AT	TACA	AGGC	AGT'	TATC'	TCA	TTGC	TGTTTT	2283
GGG	AGAG	GAA	CGGG.	AAAA	GC T	rrrr(GCTT	А ТТ'	TGTC'	TTTT	GAA	TTAA	AAG	GCTG	GGCGCG	2343
GTG	GCTC	ACA	CCTG	TAAT	CC C	AGCA	CTTT	G AG	AGGA'	TGAG	GTA	GGCG	GAT	CACT	GGGGTC	2403
AGG	ATTT	CGA	GACC	AGCC	TG G	CCAA	CATG	G CG	AAAC	CTCG	CCT	CTAC'	TAA .	AAAT.	ACAAAA	2463
AAA	TTAG	CTG	CGCG	TGGT	GG T	GCAC	GCCT	G TA	GTCC	CTGC	TAC	TTGG.	AAG	GCTG.	AGACAG	2523
GAA	TTAA	GCT	TGAG	CCCA	GG A	GGCT	GAGG'	T TG	CAGT	GAGC	CAG	GATT	GCG	CCAC	CACACT	2583
CCA	GCCT	GGG	CAAC	AGAG	AC T	CTGT	CTCA	A AA	AAAA	AAAA	AAA	AAAA				2630

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 715 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
- Met Ala Arg Glu Leu Tyr His Glu Glu Phe Ala Arg Ala Gly Lys Gln
 5 10 15
- Ala Gly Leu Gln Val Trp Arg Ile Glu Lys Leu Glu Leu Val Pro Val 20 25 30
- Pro Gln Ser Ala His Gly Asp Phe Tyr Val Gly Asp Ala Tyr Leu Val
- Leu His Thr Ala Lys Thr Ser Arg Gly Phe Thr Tyr His Leu His Phe 50 55 60
- Trp Leu Gly Lys Glu Cys Ser Gln Asp Glu Ser Thr Ala Ala Ala Ile
 65 70 75 80
- Phe Thr Val Gln Met Asp Asp Tyr Leu Gly Gly Lys Pro Val Gln Asn 85 90 95
- Arg Glu Leu Gln Gly Tyr Glu Ser Asn Asp Phe Val Ser Tyr Phe Lys
 100 105 110
- Gly Gly Leu Lys Tyr Lys Ala Gly Gly Val Ala Ser Gly Leu Asn His 115 120 125
- Val Leu Thr Asn Asp Leu Thr Ala Lys Arg Leu Leu His Val Lys Gly 130 135 140
- Arg Arg Val Val Arg Ala Thr Glu Val Pro Leu Ser Trp Asp Ser Phe 145 150 155 160
- Asn Lys Gly Asp Cys Phe Ile Ile Asp Leu Gly Thr Glu Ile Tyr Gln 165 170 175
- Trp Cys Gly Ser Ser Cys Asn Lys Tyr Glu Arg Leu Lys Ala Asn Gln 180 185 190
- Val Ala Thr Gly Ile Arg Tyr Asn Glu Arg Lys Gly Arg Ser Glu Leu 195 200 205
- Ile Val Val Glu Glu Gly Ser Glu Pro Ser Glu Leu Ile Lys Val Leu 210 215 220
- Gly Glu Lys Pro Glu Leu Pro Asp Gly Gly Asp Asp Asp Asp Ile Ile 225 230 235 240
- Ala Asp Ile Ser Asn Arg Lys Met Ala Lys Leu Tyr Met Val Ser Asp 245 250 255
- Ala Ser Gly Ser Met Arg Val Thr Val Val Ala Glu Glu Asn Pro Phe

Ser	Met	Ala 275	Met	Leu	Leu	Ser	Glu 280	Glu	Суѕ	Phe	Ile	Leu 285	Asp	His	Gly
Ala	Ala 290	Lys	Gln	Ile	Phe	Val 295	Trp	Lys	Gly	Lys	Asp 300	Ala	Asn	Pro	Gln
Glu 305	Arg	Lys	Ala	Ala	Met 310		Thr	Ala	Glu	Glu 315	Phe	Leu	Gln	Gln	Met 320
Asn	Tyr	Ser	Lys	Asn 325	Thr	Gln	Ile	Gln	Val 330	Leu	Pro	Glu	Gly	Gly 335	Glu
Thr	Pro	Ile	Phe 340	Lys	Gln	Phe	Phe	Lys 345	Asp	Trp	Arg	Asp	Lys 350	Asp	Gln
Ser	Asp	Gly 355	Phe	Gly	Lys	Val	Tyr 360	Val	Thr	Glu	Lys	Val 365	Ala	Gln	Ile
Lys	Gln 370	Ile	Pro	Phe	Asp	Ala 375	Ser	Lys	Leu	His	Ser 380	Ser	Pro	Gln	Met
Ala 385	Ala	Gln	His	Asn	Met 390	Val	Asp	Asp	Gly	Ser 395	Gly	Lys	Val	Glu	Ile 400
Trp	Arg	Val	Glu	Asn 405	Asn	Gly	Arg	Ile	Gln 410	Val	Asp	Gln	Asn	Ser 415	Tyr
Gly	Glu	Phe	Tyr 420	Gly	Gly	Asp	Cys	Tyr 425	Ile	Ile	Leu	Tyr	Thr 430	Tyr	Pro
Arg	Gly	Gln 435	Ile	Ile	Tyr	Thr	Trp 440	Gln	Gly	Ala	Asn	Ala 445	Thr	Arg	Asp
Glu	Leu 450	Thr	Thr	Ser	Ala	Phe 455	Leu	Thr	Val	Gln	Leu 460	Asp	Arg	Ser	Leu
Gly 465	Gly	Gln	Ala	Val	Gln 470	Ile	Arg	Val	Ser	Gln 475	Gly	Lys	Glu	Pro	Val 480
His	Leu	Leu	Ser	Leu 485	Phe	Lys	Asp	Lys	Pro 490	Leu	Ile	Ile	Tyr	Lys 495	Asn
Gly	Thr	Ser	Lys 500	Lys	Gly	Gly	Gln	Ala 505	Pro	Ala	Pro	Pro	Thr 510	Arg	Leu
Phe	Gln	Val 515	Arg	Arg	Asn	Leu	Ala 520	Ser	Ile	Thr	Arg	11e 525	Val	Glu	Val
Asp	Val 530	Asp	Ala	Asn	Ser	Leu 535	Asn	Ser	Asn	Asp	Val 540	Cys	Val	Leu	Lys
Leu 545	Pro	Gln	Asn	Ser	Gly 550	Tyr	Ile	Trp	Val	Gly 555	Lys	Gly	Ala	Ser	Gln 560
Glu	Glu	Glu	Lys	Gly 565	Ala	Glu	Tyr	Val	Ala 570	Ser	Val	Leu	Lys	Cys 575	Lys
Thr	Leu	Arg	Île 580	Gln	Glu	Gly	Glu	Glu 585	Pro	Glu	Glu	Phe	Trp 590	Asn	Ser

Leu Gly Gly Lys Lys Asp Tyr Gln Thr Ser Pro Leu Leu Glu Thr Gln 595 600 605

Ala Glu Asp His Pro Pro Arg Leu Tyr Gly Cys Ser Asn Lys Thr Gly 610 620

Arg Phe Val Ile Glu Glu Ile Pro Gly Glu Phe Thr Gln Asp Asp Leu 625 630 635

Ala Glu Asp Asp Val Met Leu Leu Asp Ala Trp Glu Gln Ile Phe Ile 645 650 655

Trp Ile Gly Lys Asp Ala Asn Glu Val Glu Lys Lys Glu Ser Leu Lys 660 665 670

Ser Ala Lys Met Tyr Leu Glu Thr Asp Pro Ser Gly Arg Asp Lys Arg 675 680 685

Thr Pro Ile Val Ile Ile Lys Gln Gly His Glu Pro Pro Thr Phe Thr 690 695 700

Gly Trp Phe Leu Gly Trp Asp Ser Ser Lys Trp
705 710 715

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Asn His Val Leu Thr Asn Asp Leu Thr Ala Lys Arg Leu His 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Val Tyr Val Thr Glu Lys Val Ala Gln Ile Lys Gln Ile Pro Phe

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
- Met Ala Pro His Arg Pro Ala Pro Ala Leu Leu Cys Ala Leu Ser Leu
 1 10 15
- Ala Leu Cys Ala Leu Ser Leu Pro Val Arg Ala Ala Thr Ala Ser Arg 20 25 30
- Gly Ala Ser Gln Ala Gly Ala Pro Gln Gly Arg Val Pro Glu Ala Arg
- Pro Asn Ser Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys 50 55 60
- Glu Pro Gly Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro 65 70 75 80
- Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val 85 90 95
- Ile Leu Lys Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu 100 105 110
- His Tyr Trp Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala 115 120 125
- Ala Ile Phe Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val 130 135 140
- Gln His Arg Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr 145 150 155 160
- Phe Lys Ser Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe 165 170 175
- Lys His Val Val Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val
- Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Glu 195 200 205
- Ser Phe Asn Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile 210 215 220
- His Gln Trp Cys Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala 225 230 235 240

Thr	Gln	Val	Ser	Lys 245	Gly	Ile	Arg	Asp	Asn 250	Glu	Arg	Ser	Gly	Arg 255	Ala .
Arg	Val	His	Val 260	Ser	Glu	Glu	Gly	Thr 265	Glu	Pro	Glu	Ala	Met 270	Leu	Gln
Val	Leu	Gly 275	Pro	Lys	Pro	Ala	Leu 280	Pro	Ala	Gly	Thr	Glu 285	Asp	Thr	Ala
Lys	Glu 290	Asp	Ala	Ala	Asn	Arg 295	Lys	Leu	Ala	Lys	Leu 300	Tyr	Lys	Val	Ser
Asn 305	Gly	Ala	Gly	Thr	Met 310	Ser	Val	Ser	Leu	Val 315	Ala	Asp	Glu	Asn	Pro 320
	Ala			325				٠	330					335	
-	Lys		340					345		•			350		
	Glu	355					360					365			
	Asp 370	••				375					380				
Glu 385	Thr	Pro	Leu	Phe	Lys 390	Gln	Phe	Phe	Lys	Asn 395	Trp	Arg	Asp	Pro	Asp 400
Gln	Thr	Asp	Gly	Leu 405	Gly	Leu	Ser	Tyr	Leu 410	Ser	Ser	His	Ile	Ala 415	Asn
Val	Glu	Arg	Val 420	Pro	Phe	Asp	Ala	Ala 425	Thr	Leu	His	Thr	Ser 430	Thr	Ala
Met	Ala	Ala 435		His	Gly	Met	Asp 440	Asp	Asp	Gly	Thr	Gly 445	Gln	Lys	Gln
Ile	Trp 450	Arg	Ile	Glu	Gly	Ser 455	Asn	Lys	Val	Pro	Val 460	Asp	Pro	Ala	Thr
Tyr 465	Gly	Gln	Phe	Tyr	Gly 470	Gly	Asp	Ser	Tyr	Ile 475	Ile	Leu	Tyr	Asn	Tyr 480
Arg	His	Gly	Gly	Arg 485	Gln	Gly	Gln	Ile	11e 490	Tyr	Asn	Trp	Gln	Gly 495	Ala
Gln	Ser	Thr	Gln 500	Asp	Glu	Val	Ala	Ala 505	Ser	Ala	Ile	Leu	Thr 510	Ala	Gln
Leu	Asp	Glu 515		Leu	Gly	Gly	Thr 520	Pro	Val	Gln	Ser	Arg 525	Val	Val	Gln
Gly	Lys 530		Pro	Ala	His	Leu 535	Met	Ser	Leu	Phe	Gly 540	Gly	Lys	Pro	Met
Ile 545	Ile	Tyr	Lys	Gly	Gly 550	Thr	Ser	Arg	Glu	Gly 555	Gly	Gln	Thr	Ala	Pro 560

Ala Ser Thr Arg Leu Phe Gln Val Arg Ala Asn Ser Ala Gly Ala Thr 565 570 575

Arg Ala Val Glu Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp 580 585 590

Ala Phe Val Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr 595 600 605

Gly Ala Ser Glu Ala Glu Lys Thr Gly Ala Gln Glu Leu Leu Arg Val 610 615 620

Leu Arg Ala Gln Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly 625 630 635 640

Phe Trp Glu Ala Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg 645 650 655

Leu Lys Asp Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys
660 665 670

Ser Asn Lys Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu 675 680 685

Met Gln Glu Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp 690 695 700

Asp Gln Val Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys 705 710 715 720

Thr Glu Ala Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala 725 730 735

Asn Arg Asp Arg Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu
740 745 750

Pro Pro Ser Phe Val Gly Trp Phe Leu Gly Trp Asp Asp Tyr Trp 755 760 765

Ser Val Asp Pro Leu Asp Arg Ala Met Ala Glu Leu Ala Ala 770 775 780

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 827 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Thr Lys Leu Ser Ala Gln Val Lys Gly Ser Leu Asn Ile Thr Thr 1 5 10 15

Pro Gly Leu Gln Ile Trp Arg Ile Glu Ala Met Gln Met Val Pro Val

25

Leu Ala Ile His Lys Thr Ala Ser Ser Leu Ser Tyr Asp Ile His Tyr 50 55 60

Trp Ile Gly Gln Asp Ser Ser Leu Asp Glu Gln Gly Ala Ala Ala Ile 65 70 75 80

Tyr Thr Thr Gln Met Asp Asp Phe Leu Lys Gly Arg Ala Val Gln His 85 90 95

Arg Glu Val Gln Gly Asn Glu Ser Glu Ala Phe Arg Gly Tyr Phe Lys 100 105 110

Gln Gly Leu Val Ile Arg Lys Gly Gly Val Ala Ser Gly Met Lys His 115 120 125

Val Glu Thr Asn Ser Tyr Asp Val Gln Arg Leu Leu His Val Lys Gly 130 135 140

Lys Arg Asn Val Val Ala Gly Glu Val Glu Met Ser Trp Lys Ser Phe 145 150 155 160

Asn Arg Gly Asp Val Phe Leu Leu Asp Leu Gly Lys Leu Ile Ile Gln 165 170 175

Trp Asn Gly Pro Glu Ser Thr Arg Met Glu Arg Leu Arg Gly Met Thr 180 185 190

Leu Ala Lys Glu Ile Arg Asp Gln Glu Arg Gly Gly Arg Thr Tyr Val 195 200 205

Gly Val Val Asp Gly Glu Asn Glu Leu Ala Ser Pro Lys Leu Met Glu 210 215 220

Val Met Asn His Val Leu Gly Lys Arg Arg Glu Leu Lys Ala Ala Val 225 230 235 240

Pro Asp Thr Val Val Glu Pro Ala Leu Lys Ala Ala Leu Lys Leu Tyr 245 250 255

His Val Ser Asp Ser Glu Gly Asn Leu Val Val Arg Glu Val Ala Thr 260 265 270

Arg Pro Leu Thr Gln Asp Leu Leu Ser His Glu Asp Cys Tyr Ile Leu 275 280 285

Asp Gln Gly Gly Leu Lys Ile Tyr Val Trp Lys Gly Lys Lys Ala Asn 290 295 300

Glu Gln Glu Lys Lys Gly Ala Met Ser His Ala Leu Asn Phe Ile Lys 305 310 315 320

Ala Lys Gln Tyr Pro Pro Ser Thr Gln Val Glu Val Gln Asn Asp Gly 325 330 335

Ala Glu Ser Ala Val Phe Gln Gln Leu Phe Gln Lys Trp Thr Ala Ser 340 345 350

Asn	Arg	Thr 355	Ser	Gly	Leu	Gly	Lys 360	Thr	His	Thr	Val	Gly 365		Val	Ala
Lys	Val 370	Glu	Gln	Val	Lys	Phe 375	Asp	Ala	Thr	Ser	Met 380	His	Val	Lys	Pro
Gln 385	Val	Ala	Ala	Gln	Gln 390	Lys	Met	Val		Asp 395	Gly	Ser	Gly	Glu	Val 400
Gln	Val	Trp	Arg	Ile 405	Glu	Asn	Leu	Glu	Leu 410	Val	Pro	Val	Asp	Ser 415	Lys
Trp	Leu	Gly	His 420	Phe	Tyr	Gly	Gly	Asp 425	Cys	Tyr	Leu	Leu	Leu 430	Tyr	Thr
Tyr	Leu	Ile 435	Gly	Glu	Lys	Gln	His 440	Tyr	Leu	Leu	Tyr	Val 445	Trp	Gln	Gly
Ser	Gln 450	Ala	Ser	Gln	Asp	Glu 455	Ile	Thr	Ala	Ser	Ala 460	Tyr	Gln	Ala	Val
Ile 465	Leu	Asp	Gln	Lys	Tyr 470	Asn	Gly	Glu	Pro	Val 475	Gln	Ile	Arg	Val	Pro 480
Met	Gly	Lys	Glu	Pro 485	Pro	His	Leu	Met	Ser 490	Ile	Phe	Lys	Gly	Arg 495	Met
Val	Val	Tyr	Gln 500	Gly	Gly	Thr	Ser	Arg 505	Thr	Asn	Asn	Leu	Glu 510	Thr	Gly
Pro	Ser	Thr 515	Arg	Leu	Phe	Gln	Val 520	Gln	Gly	Thr	Gly	Ala 525	Asn	Asn	Thr
Lys	Ala 530	Phe	Glu	Val	Pro	Ala 535	Arg	Ala	Asn	Phe	Leu 540	Asn	Ser	Asn	Asp
Val 545	Phe	Val	Leu	Lys	Thr 550	Gln	Ser	Cys	Суѕ	Tyr 555	Leu	Trp	Суѕ	Gly	Lys 560
Gly	Cys	Ser	Gly	Asp 565	Glu	Arg	Glu	Met	Ala 570	Lys	Met	Val	Ala	Asp 575	Thr
Ile	Ser	Arg	Thr 580	Glu	Lys	Gln	Val	Val 585	Val	Glu	Gly	Gln	Glu 590	Pro	Ala
Asn	Phe	Trp 595	Met	Ala	Leu	Gly	Gly 600	Lys	Ala	Pro	Tyr	Ala 605	Asn	Thr	Lys
Arg	Leu 610	Gln	Glu	Glu	Asn	Leu 615	Val	Ile	Thr	Pro	Arg 620	Leu	Phe	Glu	Cys
Ser 625	Asn	Lys	Thr	Gly	Arg 630	Phe	Leu	Ala	Thr	Glu 635	Ile	Pro	Asp	Phe	Asn 640
Gln	Asp	Asp	Leu	Glu 645	Glu	Asp	Asp	Val	Phe 650	Leu	Leu	Asp	Val	Trp 655	Asp
Gln	Val	Phe	Phe 660	Trp	Ile	Gly	Lys	His 665	Ala	Asn	Glu	Glu	Glu 670	Lys	Lys

Ala	Ala	Ala 675	Thr	Thr	Ala	Gln	Glu 680	Tyr	Leu	Lys	Thr	His 685	Pro	Ser	Gly
Arg	Asp 690	Pro	Glu	Thr	Pro	Ile 695	Ile	Val	Val	Lys	Gln 700	Gly	His	Glu	Pro
Pro 705	Thr	Phe	Thr	Gly	Trp 710	Phe	Leu	Ala	Trp	Asp 715	Pro	Phe	Lys	Trp	Ser 720
Asn	Thr	Lys	Ser	Tyr 725	Glu	Asp	Leu	Lys	Ala 730	Glu	Ser	Gly	Asn	Leu 735	Arg
Asp	Trp	Ser	Gln 740	Ile	Thr	Ala	Glu	Val 745	Thr	Ser	Pro	Lys	Val 750	Asp	Val
Phe	Asn	Ala 755	Asn	Ser	Asn	Leu	Ser 760	Ser	Gly	Pro	Leu	Pro 765	Ile	Phe	Pro
Leu	Glu 770	Gln	Leu	Val	Asn	Lys 775	Pro	Val	Glu	Glu	Leu 780	Pro	Glu	Gly	Val
Asp 785	Pro	Ser	Arg	Lys	Glu 790	Glu	His	Leu	Ser	Ile 795	Glu	Asp	Phe	Thr	Gln 800
Ala	Phe	Gly	Met	Thr 805	Pro	Ala	Ala	Phe	Ser 810	Ala	Leu	Pro	Arg	Trp 815	Lys
Gln	Gln	Asn	Leu 820	Lys	Lys	Glu	Lys	Gly 825	Leu	Phe					

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "PRIMER"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATGCGGATC CAAYGAYYTN ACNGCNCA

- (2) INFORMATION FOR SEQ ID NO:13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
GATGCATCGA TACRTGNGCN ACYTTYTC	28
(2) INFORMATION FOR SEQ ID NO:14:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
CTCGAGGGTG GCGACGACTC C	21
(2) INFORMATION FOR SEQ ID NO:15:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 23 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
GCGGCCGCTT GACACCAGAC CAA	23
(2) INFORMATION FOR SEQ ID NO:16:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 24 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER"</pre>	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

- (2) INFORMATION FOR SEQ ID NO:17:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "PRIMER"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
 ACGACGGCCA GTGAATTGCG TAAT
- (2) INFORMATION FOR SEQ ID NO:18:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys Val Ala Lys Val Glu Gln Val Lys Phe Asp Ala 1 5 10 Sequence Listing

SEQ ID NO:

Sequence length: 12

Sequence Type: amino acid

5 Topology: linear

Molecule type: peptide

Sequence description: KVAHVKQIPFDA

SEQ ID NO: 2

10 Sequence length: 9

Sequence Type: amino acid

Topology: linear

Molecule type: peptide

Sequence description: VLTNDLTAQ

15

SEQ ID NO:

Sequence length: 5

Sequence Type: amino acid

Topology: linear

20 Molecule type: peptide

Sequence description: ITNRK

SEQ ID NO: 4

Sequence length: 2418

25 Sequence Type: nucleic acid

Strandeness: double

Topology: linear

1 - - 53 - 22...car

Molecule type: cDNA

Sequence characteristic:

Symbol Showing Characteristic: mat peptide

Location: 27. . 2171

Sequence description:

		CCCC	200G2	VAC A	ATCGC	GTGC	.c cc	AGTO		Ala				Tyr	CAC His	47
GAG Glu	GAC Glu	TTC Phe	e Ala	CGC Arg	GCC Ala	GCC Gly	: AAC Lys 15	Arg	GCG Ala	Gly	CIG Leu	CAG Gln 20	GTC Val	TCG	AGA Arg	95
ATT	GAG Glu 25	Lys	CIG Leu	GAG Glu	CIG Leu	GIG Val 30	Pro	GTG	CCC Pro	GAG Glu	AGC Ser 35	GCG Ala	TAT Tyr	Gly	AAC Asn	143
TTC Phe 40	TAC Tyr	GTC Val	: ccc : Gly	GAT Asp	GCC Ala 45	TAC Tyr	CIG Leu	GTG Val	CTC	CAC His 50	ACG Thr	ACG Thr	CAG Gln	GCC Ala	AGC Ser 55	191
CGG Arg	Gly	TTC Phe	ACC	TAC Tyr 60	Arg	CIG Læu	CAC His	TTC Phe	TGG Trp 65	CTG Leu	GGA Gly	AAG Lys	GAG Glu	TGT Cys 70	ACT Thr	239
CAG Gln	CAT Asp	GAA Glu	AGC Ser 75	ACA Thr	GCA Ala	GCT Ala	GCC Ala	ATC Ile 80	TTT Phe	ACT Thr	GTT Val	CAG Gln	ATG Met 85	GAT Asp	GAC Asp	287
												CAA Gln 100				335
TCT Ser	ACG Thr 105	GAT Asp	TTT Phe	GIT Val	Gly	TAC Tyr 110	TIT Phe	AAA Lys	GGA Gly	GT Gly	CTG Leu 115	AAA Lys	TAC Tyr	AAG Lys	GCT Ala	383
GGC Gly 120	GT Gly	GTG Val	GCG Ala	TCT Ser	GGA Gly 125	CTC Leu	TAA Asn	CAT His	GIG Val	CTT Leu 130	ACA Thr	TAA Asn	GAC Asp	TIG Leu	ACT Thr 135	431
												GTC Val				479
												GAC Asp				527
	Asp											TCT Ser				575

AA	الآل ف	M ()	AG (JGC (CIG	AA	G GC	C A	SC C	ΆG	GT.	r GO	C AT	\mathcal{L}	SC A	ידו	3G G24	√C 623
Ly	s Ty 18	/I G.	lu A	arg 1	Leu	Lys	s Al 19	.a Se	er G	Jn	Val	L Al	a Il 19	.e G]	ly I	le Aı	JU GA Tg As	p 623
AAT Asi 200	ו טו	A A(u Ar	G A	AA (ys (Sly	AGA Arg 205	JAL	T C? a Gl	n r & c	TG eu	ATI Ile	CTC Val	l Va	A G2 l Gl	A GA u Gl	AA CC .u Gl	SG AG .y Se 21	r
GAA Glu	A CC 1 Pro	A TO O Se	A G r G	TU L	ETT Æu 20	ACA Thr	AA Ly:	G GI s Va	A T	eu (033 Gly 225	GA? Glu	AAA 1 Ly:	G CC s Pr	A AA O Ly	G CI 's Le 23	T AC U Ari O	G 719 J
GAT Asp	Gly	A GA y Gl	u A	AT G Sp A 35	ed Sed	GAT Asp	, Gy Yei	C AT	C AA e L <u>y</u> 24	s A	GCA Ala	GAI	ATT	A AC	T AA r As 24	n An	G AAJ g Lys	A 767
ATG Met	GCT Ala	r aa a Ly: 25	s Le	C T	AC : YI 1	ATG Met	GT Val	TC: Se: 25:	r As	T. A. q.	SCC Na	AGT Ser	Gly GGC	TC(Ser 26(Me	G AAI t Ly:	A GIG s Val	815
AGT Ser	CTC Leu 265	ı va	G GC l Al	IA GI .a GI	AA (lu (GAA Glu	AAC Asn 270	Pro	O Ph	C I	.cc er	ATG Met	GCG Ala 275	Met	CT Lea	r CTO	G TCI 1 Ser	863
GAA Glu 280	GAA Glu	. TG(Cys	Ç TI 5 Ph	C AI	le I	TTG Leu 285	GAC Asp	CAC His	GG GG	T G Y A	la	GCA Ala 290	AAA Lys	CAG Gln	ATI	TTT Phe	GIA Val 295	911
TCG Trp	AAA Lys	Gly	AA Ly	A CA S As 30	D A	XT Ja	AAT ASN	CCC	CA(ı G	AG . lu . 05	AGA Arg	AAG Lys	GCT Ala	Ala ACC	ATG Met	AAG Lys	959
ACA Thr	GCT Ala	GAG Glu	GAI Glu 315	ו Ph	c c	TA eu (CAG Gln	CAA Gln	ATO Met	: A	AT 1	IAT Iyr	TCT Ser	ACG Thr	AAT Asn 325	Thr	CAA Gln	1007
ATT (CAA Gln	GTT Val 330	CT Le	r cc ı Pr	A G	AA (lu (GGA. Gly	ŒT Gly 335	GA2 Glu	A. A.C 1 Ti	CA (r !	CCA Pro	ATC	TTC Phe 340	AAA Lys	CAG Gln	TTC Phe	1055
ITT / Phe I	AAG Lys 345	GAC Asp	TCC Trp	AG Arg	A G	SD A	AGA Arg 850	GAT Asp	CAG Gln	AC Se	SC C	de/	GGC Gly 355	TTC Phe	GJY GGG	AAA Lys	GTG Val	1103
PAT (Tyr 1	IC . Val	ACA Thr	GAA Glu	AA/	A G1 s Va 36	al A	CT Lla	CAC His	GTA Val	AA Ly	's G	AA 2 31n :	ATT	CCA Pro	TTT Phe	GAT Asp	GCC Ala	1151

Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala Gln His His Val Val 380 385 385 390 390 390 385 385 390 390 390 390 385 385 385 390	Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala Gln His His Val Val 380 385 390 GAT GAC GGT TCT GGC AAA GTG CAG ATT TGG CGT GTA GAA AAC AAC GGT 1247 Asp Asp Gly Ser Gly Lys Val Gln Ile Trp Arg Val Glu Asn Asn Gly 395 400 405 AGG GTC GAA ATT GAC CGA AAC TGG TAT GGT GAA TTC TAT GGT GGT GAT 1295 Arg Val Glu Ile Asp Arg Asn Ser Tyr Gly Glu Phe Tyr Gly Gly Asp 410 415 420 TGC TAC ATT ATA CTT TAC ACT TAT CCC AGA GGA CAG ATT ATC TAC ACC 1343 Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro Arg Gly Gln Ile Ile Tyr Thr 425 430 435 TGG CAA GGA GCA AAT GCC ACA CGG GAT GAG CTG ACA ACC TCC GCA TTC 1391 Trp Gln Gly Ala Asn Ala Thr Arg Asp Glu Leu Thr Thr Ser Ala Phe 440 445 450 455 CTG ACT GTT CAG TTG GAT AGA TCC CTC GGG GGA CAG GCT GTG CAG ATT 1439										·		
Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala Gln His His Val 390 GAT GAC GGT TCT GGC AAA GTG CAG ATT TGG CGT GTA GAA AAC AAC GGT Asp Asp Gly Ser Gly Lys Val Gln Ile Trp Arg Val Glu Asn Asn GIY 400 AGG GTC GAA ATT GAC CGA AAC TGG TAT GGT GAA TTC TAT GGT GGT GAT Arg Val Glu Ile Asp Arg Asn Ser Tyr Gly Glu Phe Tyr Gly Gly Asp 410 TGC TAC ATT ATA CTT TAC ACT TAT TYR Tyr Pro Arg Gly Gln Ile Ile Tyr Thr 425 TGG CAA GCA GCA AAT GCC ACA CGG GAT GAG CTG ACA ACC TCC GCA TTC Trp Gln Gly Ala Asn Ala Thr Arg Asp Glu Leu Thr Thr Ser Ala Phe 440 CTG ACT GTT CAG TTG GAT AGA TCC CTC GGG GGA CAG CTG GTG CAG ATT Leu Thr Val Gln Leu Asp Arg Ser Leu Gly Gly Gln Ala Val Gln Ile Leu Thr Val Gln Gly Lys Glu Pro Ala His Leu Leu Ser Leu Phe Lys 475 GAC AAA CGG CTC ATT ATT TAC ACG GGT CAC CTG CTG GGT GTG CAG ATT TC AAC ACG GTG GTG CAG ATT THE AAG ACG GTC GTG CAG ATT TO AAA Arg Val Ser Gln Gly Lys Glu Pro Ala His Leu Leu Ser Leu Phe Lys 475 GAC AAA CGG CTC ATT ATT TAC AAG AAC GGA ACA TCA AAC GGT GTG CAG ATT TAC AAC AAC GGT GTG CAG ATT TC TY Val Ser Gln Gly Lys Glu Pro Ala His Leu Leu Ser Leu Phe Lys 480 GAC AAA CGG CTC ATT ATT TAC AAG AAC GGA ACA TCA AAG AAA GAA GGT Asp Lys Pro Leu Ile Ile Tyr Lys Asn Gly Thr Ser Lys Lys Glu Gly Asp 490	Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala Gln His His Val Val 380 385 390 GAT GAC GGT TCT GGC AAA GTG CAG ATT TGG CGT GTA GAA AAC AAC GGT ASp Asp Gly Ser Gly Lys Val Gln Ile Trp Arg Val Glu Asn Asn Gly 400 405 AGG GTC GAA ATT GAC CGA AAC TCG TAT GGT GAA TTC TAT GGT GGT GAT Arg Val Glu Ile Asp Arg Asn Ser Tyr Gly Glu Phe Tyr Gly Gly Asp 410 415 420 TGC TAC ATT ATA CTT TAC ACT TAT CCC AGA GGA CAG ATT ATC TAC ACC Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro Arg Gly Gln Ile Ile Tyr Thr 425 430 435 TGG CAA GGA GCA AAT GCC ACA CGG GAT GAG CTG ACA ACC TCC GCA TTC TTP Gln Gly Ala Asn Ala Thr Arg Asp Glu Leu Thr Thr Ser Ala Phe 440 445 450 450 455 CTG ACT GTT CAG TTG GAT AGA TCC CTC GGG GGA CAG GCT GTG CAG ATT	1199	1247	1295	1343	1391	1439	1487	1535	1583		1631	1631 1679
Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala Gln His His Val 380 385 385 385 380 390 390	Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala Gln His His Val 380					Phe							Leu 535 TAC
Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala Gln His His 380	Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala Gln His His 380 385 GAT GAC GGT TCT GGC AAA GTG CAG ATT TGG CGT GTA GAA AAC Asp Asp Gly Ser Gly Lys Val Gln Ile Trp Arg Val Glu Asn 405 AGG GTC GAA ATT GAC CGA AAC TGG TAT GGT GAA TTC TAT GGT Arg Val Glu Ile Asp Arg Asn Ser Tyr Gly Glu Phe Tyr Gly 410 415 420 TGC TAC ATT ATA CTT TAC ACT TAT CGC AGA GGA CAG ATT ATC Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro Arg Gly Gln Ile Ile 425 430 435 TGG CAA GGA GCA AAT GCC ACA CGG GAT GAG CTG ACA ACC TCC Trp Gln Gly Ala Asn Ala Thr Arg Asp Glu Leu Thr Thr Ser 440 445 450 CTG ACT GTT CAG TTG GAT AGA TCC CTC GGG GGA CAG GCT GTG	Val	AAC			Ala	Gln					TCA Ser	TCA
Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala Gln His 380 GAT GAC GGT TCT GGC AAA GTG CAG ATT TGG CGT GTA GAA ASp Asp Gly Ser Gly Lys Val Gln Ile Trp Arg Val Glu 395 AGG GTC GAA ATT GAC CGA AAC TGG TAT GGT GAA TTC TAT A10 A10	Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala Gln His 380 385 GAT GAC GGT TCT GGC AAA GTG CAG ATT TGG CGT GTA GAA ASp Asp Gly Ser Gly Lys Val Gln Ile Trp Arg Val Glu 395 400 AGG GTC GAA ATT GAC CGA AAC TGG TAT GGT GAA TTC TAT Arg Val Glu Ile Asp Arg Asn Ser Tyr Gly Glu Phe Tyr 410 415 425 TGC TAC ATT ATA CTT TAC ACT TAT CCC AGA GGA CAG ATT Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro Arg Gly Gln Ile 425 430 435 TGG CAA GGA GCA AAT GCC ACA CGG GAT GAG CTG ACA ACC Trp Gln Gly Ala Asn Ala Thr Arg Asp Glu Leu Thr Thr 440 445 450 CTG ACT GTT CAG TTG GAT AGA TCC CTC GGG GGA CAG GCT		Asn					Leu			5	AAC	AAC Asn AAT
Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala Gln 380 GAT GAC GGT TCT GGC AAA GTG CAG ATT TGG CGT GTA Asp Asp Gly Ser Gly Lys Val Gln Ile Trp Arg Val 395 AGG GTC GAA ATT GAC CGA AAC TGG TAT GGT GAA TTC Arg Val Glu Ile Asp Arg Asn Ser Tyr Gly Glu Phe 410 TGC TAC ATT ATA CTT TAC ACT TAT CCC AGA GGA CAG Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro Arg Gly Gln 425 TGG CAA GGA GCA AAT GCC ACA CGG GAT GAG CTG ACA Trp Gln Gly Ala Asn Ala Thr Arg Asp Glu Leu Thr 440 CTG ACT GTT CAG TTG GAT AGA TCC CTC GGG GGA CAG Leu Thr Val Gln Leu Asp Arg Ser Leu Gly Gly Gln 460 CGA GTC TCC CAA GGC AAA GAA GAA CCT GCT CAC CTG CTG Arg Val Ser Gln Gly Lys Glu Pro Ala His Leu Leu 475 GAC AAA CGG CTC ATT ATT TAC AAG AAC GGA ACA TCA Asp Lys Pro Leu Ile Ile Tyr Lys Asn Gly Thr Ser 490	Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala Gln 380 GAT GAC GGT TCT GGC AAA GTG CAG ATT TGG CGT GTA Asp Asp Gly Ser Gly Lys Val Gln Ile Trp Arg Val 395 AGG GTC GAA ATT GAC CGA AAC TCG TAT GGT GAA TTC Arg Val Glu Ile Asp Arg Asn Ser Tyr Gly Glu Phe 410 TGC TAC ATT ATA CTT TAC ACT TAT CCC AGA GGA CAG Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro Arg Gly Gln 425 TGG CAA GGA GCA AAT GCC ACA CGG GAT GAG CTG ACA Trp Gln Gly Ala Asn Ala Thr Arg Asp Glu Leu Thr 440 CTG ACT GTT CAG TTG GAT AGA TCC CTC GGG GGA CAG		Glu	ŢŢ				Ser	Lys		мg	GCA	GCA Ala AAT
Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala 385 GAT GAC GGT TCT GGC AAA GTG CAG ATT TGG CGT Asp Asp Gly Ser Gly Lys Val Gln Ile Trp Arg 400 AGG GTC GAA ATT GAC CGA AAC TCG TAT GGT GAA ATG Val Glu Ile Asp Arg Asn Ser Tyr Gly Glu 415 TGC TAC ATT ATA CTT TAC ACT TAT CCC AGA GGA CCA Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro Arg Gly 425 TGG CAA GGA GCA AAT GCC ACA CGG GAT GAG CTG TAT GGT GAA AGO CTG GAA AGO CTG GAA AGO CTG GAA AGO CTG AGA GGA AGO AGA GGA AGA CGG GAT GAG CTG AGA GGA AGO AGA GGA AGO AGA GGA AGO AGA CGG GAT GAG CTG AGO CTG AGA GGA AGO AGA GGA AGO AGA CGG GAT GAG CTG AGO AGO AGO AGO AGO AGO AGO AGO AGO AG	Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala 380 GAT GAC GGT TCT GGC AAA GTG CAG ATT TGG CGT Asp Asp Gly Ser Gly Lys Val Gln Ile Trp Arg 395 AGG GTC GAA ATT GAC CGA AAC TGG TAT GGT GAA Arg Val Glu Ile Asp Arg Asn Ser Tyr Gly Glu 410 TGC TAC ATT ATA CTT TAC ACT TAT CCC AGA GGA Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro Arg Gly 425 TGG CAA GGA GCA AAT GCC ACA CGG GAT GAG CTG Trp Gln Gly Ala Asn Ala Thr Arg Asp Glu Leu 440 CTG ACT GTT CAG TTG GAT AGA TCC CTC GGG GGA				Gln				Ser		515	515 GAT	515 GAT Asp CAA
Ser Lys Leu His Ser Ser Pro Gln Met Ala 385 GAT GAC GGT TCT GGC AAA GTG CAG ATT TGG ASP ASP Gly Ser Gly Lys Val Gln Ile Trp 400 AGG GTC GAA ATT GAC CGA AAC TGG TAT GGT ATG GLY ALO	Ser Lys Leu His Ser Ser Pro Gln Met Ala 380 GAT GAC GGT TCT GGC AAA GTG CAG ATT TGG Asp Asp Gly Ser Gly Lys Val Gln Ile Trp 395 AGG GTC GAA ATT GAC CGA AAC TGG TAT GGT ATG Val Glu Ile Asp Arg Asn Ser Tyr Gly 410 TGC TAC ATT ATA CTT TAC ACT TAT CCC AGA Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro Arg 425 TGG CAA GGA GCA AAT GCC ACA CGG GAT GAG Trp Gln Gly Ala Asn Ala Thr Arg Asp Glu 440 CTG ACT GTT CAG TTG GAT AGA TCC CTC GGG					Leu					GIN	GIT	GTT Val 530 CGA
Ser Lys Leu His Ser Ser Pro Gln Met 380 GAT GAC GGT TCT GGC AAA GTG CAG ATT ASp Asp Gly Ser Gly Lys Val Gln Ile 400 AGG GTC GAA ATT GAC CGA AAC TCG TAT A10 Val Glu Ile Asp Arg Asn Ser Tyr 415 TGC TAC ATT ATA CTT TAC ACT TAT CCC Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro 430 TGG CAA GGA GCA AAT GCC ACA CGG GAT Trp Gln Gly Ala Asn Ala Thr Arg Asp 445 CTG ACT GTT CAG TTG GAT AGA TCC CTC Leu Thr Val Gln Leu Asp Arg Ser Leu 460 CGA GTC TCC CAA GGC AAA GAA GAA CCT GCT Arg Val Ser Gln Gly Lys Glu Pro Ala 475 GAC AAA CCG CTC ATT ATT TAC AAG AAC ASp Lys Pro Leu Ile Ile Tyr Lys Asn 490	Ser Lys Leu His Ser Ser Pro Gln Met 380 GAT GAC GGT TCT GGC AAA GTG CAG ATT Asp Asp Gly Ser Gly Lys Val Gln Ile 395 400 AGG GTC GAA ATT GAC CGA AAC TCG TAT ATG Val Glu Ile Asp Arg Asn Ser Tyr 410 415 TGC TAC ATT ATA CTT TAC ACT TAT CCC Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro 425 430 TGG CAA GGA GCA AAT GCC ACA CGG GAT Trp Gln Gly Ala Asn Ala Thr Arg Asp 440 445 CTG ACT GTT CAG TTG GAT AGA TCC CTC	Ala					Gly				rne	GAT	GAT Asp CTG
Ser Lys Leu His Ser Ser Pro Gln 380 GAT GAC GGT TCT GGC AAA GTG CAG Asp Asp Gly Ser Gly Lys Val Gln 395 AGG GTC GAA ATT GAC CGA AAC TCG Arg Val Glu Ile Asp Arg Asn Ser 410 TGC TAC ATT ATA CTT TAC ACT TAT Cys Tyr Ile Ile Leu Tyr Thr Tyr 425 TGG CAA GGA GCA AAT GCC ACA CGG Trp Gln Gly Ala Asn Ala Thr Arg 440 CTG ACT GTT CAG TTG GAT AGA TCC Leu Thr Val Gln Leu Asp Arg Ser 460 CGA GTC TCC CAA GGC AAA GAA CCT Arg Val Ser Gln Gly Lys Glu Pro 475 GAC AAA CCG CTC ATT ATT TAC AAG Asp Lys Pro Leu Ile Ile Tyr Lys 490 CAS AAA GTG TYR Lys 490	Ser Lys Leu His Ser Ser Pro Gln 380 GAT GAC GGT TCT GGC AAA GTG CAG Asp Asp Gly Ser Gly Lys Val Gln 395 AGG GTC GAA ATT GAC CGA AAC TCG Arg Val Glu Ile Asp Arg Asn Ser 410 TGC TAC ATT ATA CTT TAC ACT TAT Cys Tyr Ile Ile Leu Tyr Thr Tyr 425 TGG CAA GGA GCA AAT GCC ACA CGG Trp Gln Gly Ala Asn Ala Thr Arg 440 CTG ACT GTT CAG TTG GAT AGA TCC		Ile					Ala			Leu	GIA	GTA Val AAA
Ser Lys Leu His Ser Ser Pro 380 GAT GAC GGT TCT GGC AAA GTG Asp Asp Gly Ser Gly Lys Val 395 AGG GTC GAA ATT GAC CGA AAC Arg Val Glu Ile Asp Arg Asn 410 TGC TAC ATT ATA CTT TAC ACT Cys Tyr Ile Ile Leu Tyr Thr 425 TGG CAA GGA GCA AAT GCC ACA Trp Gln Gly Ala Asn Ala Thr 440 CTG ACT GTT CAG TTG GAT AGA Leu Thr Val Gln Leu Asp Arg 460 CGA GTC TCC CAA GGC AAA GAA Arg Val Ser Gln Gly Lys Glu 475 GAC AAA CCG CTC ATT ATT TAC Asp Lys Pro Leu Ile Ile Tyr 490	Ser Lys Leu His Ser Ser Pro 380 GAT GAC GGT TCT GGC AAA GTG Asp Asp Gly Ser Gly Lys Val 395 AGG GTC GAA ATT GAC CGA AAC Arg Val Glu Ile Asp Arg Asn 410 TGC TAC ATT ATA CTT TAC ACT Cys Tyr Ile Ile Leu Tyr Thr 425 TGG CAA GGA GCA AAT GCC ACA Trp Gln Gly Ala Asn Ala Thr 440 CTG ACT GTT CAG TTG GAT AGA			Ser					Lys		1119	GAG	GAG Glu CIG
Ser Lys Leu His Ser Ser 380 GAT GAC GGT TCT GGC AAA ASP ASP Gly Ser Gly Lys 395 AGG GTC GAA ATT GAC CGA Arg Val Glu Ile Asp Arg 410 TGC TAC ATT ATA CTT TAC Cys Tyr Ile Ile Leu Tyr 425 TGG CAA GGA GCA AAT GCC Trp Gln Gly Ala Asn Ala 445 CTG ACT GTT CAG TTG GAT Leu Thr Val Gln Leu Asp 460 CGA GTC TCC CAA GGC AAA Arg Val Ser Gln Gly Lys 475 GAC AAA CCG CTC ATT ATT ASP Lys Pro Leu Ile Ile 490	Ser Lys Leu His Ser Ser 380 GAT GAC GGT TCT GGC AAA Asp Asp Asp Gly Ser Gly Lys 395 AGG GTC GAA ATT GAC CGA Arg Val Glu Ile Asp Arg 410 TGC TAC ATT ATA CTT TAC Cys Tyr Ile Ile Leu Tyr 425 TGG CAA GGA GCA AAT GCC Trp Gln Gly Ala Asn Ala 440 CTG ACT GTT CAG TTG GAT				Thr						510	510 ATG	510 ATG Met
Ser Lys Leu His Ser 380 GAT GAC GGT TCT GGC Asp Asp Gly 395 AGG GTC GAA ATT GAC Arg Val Glu Ile Asp 410 TGC TAC ATT ATA CTT Cys Tyr Ile Ile Leu 425 TGG CAA GGA GCA AAT Trp Gln Gly Ala Asn 440 CTG ACT GTT CAG TTG Leu Thr Val Gln Leu 460 CGA GTC TCC CAA GGC Arg Val Ser Gln Gly 475 GAC AAA CCG CTC ATT Asp Lys Pro Leu Ile 490	Ser Lys Leu His Ser 380 GAT GAC GGT TCT GGC Asp Asp Gly Ser Gly 395 AGG GTC GAA ATT GAC Arg Val Glu Ile Asp 410 TGC TAC ATT ATA CTT Cys Tyr Ile Ile Leu 425 TGG CAA GGA GCA AAT Trp Gln Gly Ala Asn 440 CTG ACT GTT CAG TTG					Ala					FIO	TTA	ATT Ile 525 TTT
Ser Lys Leu His GAT GAC GGT TCT Asp Asp Gly Ser 395 AGG GTC GAA ATT ATG Val Glu Ile 410 TGC TAC ATT ATA Cys Tyr Ile Ile 425 TGG CAA GGA GCA Trp Gln Gly Ala 440 CTG ACT GTT CAG Leu Thr Val Gln CGA GTC TCC CAA Arg Val Ser Gln 475 GAC AAA CCG CTC Asp Lys Pro Leu 490	Ser Lys Leu His GAT GAC GGT TCT Asp Asp Gly Ser 395 AGG GTC GAA ATT Arg Val Glu Ile 410 TGC TAC ATT ATA Cys Tyr Ile Ile 425 TGG CAA GGA GCA Trp Gln Gly Ala 440 CTG ACT GTT CAG	Ser					Leu				Pro	AGA	AGA Arg GTT
Ser Lys Leu GAT GAC GGT Asp Asp Gly ACG GTC GAA Arg Val Glu 410 TGC TAC ATT Cys Tyr Ile 425 TGG CAA GGA Trp Gln Gly 440 CTG ACT GTT Leu Thr Val CGA GTC TCC Arg Val Ser GAC AAA CCG Asp Lys Pro 490	Ser Lys Leu GAT GAC GGT Asp Asp Gly AGG GTC GAA Arg Val Glu 410 TGC TAC ATT Cys Tyr Ile 425 TGG CAA GGA Trp Gln Gly 440 CTG ACT GTT		Ser					Gln		ccc	Ala	ACC	ACC Thr GAT
Ser Lys GAT GAC Asp Asp ACG GTC Arg Val TCC TAC Cys Tyr 425 TCG CAA Trp Gln 440 CTG ACT Leu Thr CCGA GTC Arg Val GAC AAA Asp Lys	Ser Lys GAT GAC Asp Asp AGG GTC Arg Val TGC TAC Cys Tyr 425 TGG CAA Trp Gln 440 CTG ACT			Glu					Pro	CCA	Pro	ATC	ATC Ile AAT
Ser GAT Asp AGG Arg TGC Cys TGG Trp 440 CIG Leu CGA Arg	Ser GAT Asp AGG Arg TCC Cys TCG Trp 440 CTG				Tyr						Ala 505	505 · TCG	505 TCG Ser
						Trp					Gln	GÇT	GCT Ala 520 AAT

															œc	1775
Tyr	Val	Ala 570	Ser	Val	Leu	Lys	Cys 575	Ľ'ns	Thr	Ser	Thr	Ile 580	Gln	Glu	Gly	
															TAC	1823
Lys	Glu 585	Pro	Glu	Glu	Phe	Trp 590	Asn	Ser	Leu	Gly	Gly 595	Lys	Lys	Asp	Tyr	
															æ	1871
	Thr	Ser	Pro	Leu		Glu	Ser	Gln	Ala	Glu	Asp	His	Pro	Pro	Arg	
600					605					610					615	
CTT	TAC	GGC	TGC	TCC	AAC	AAA	ACT	GGA.	AGA	TIC	ATT	ATT	GAA	GAG	GIT	1919
Leu	Tyr	Gly	Cys		Asn	Γ⊼2	Thr	Gly	Arg	Phe	Ile	Ile	Glu	Glu	Val	
				620					625					630		
CCA.	GGA	GAG	TTC	ACC	CAG	GAT	GAT	TTA	GCA	GAA	GAT	GAT	GTC	ATG	CTG	1967
Pro	Gly	Glu	Phe	Thr	Gln	Asp	Asp		Ala	Glu	Asp	Asp	Val	Met	Leu	
			635					640					645	-		
TTA	CAT	GCT	TGG	GAA	CAG	ATT	TTT	ATT	TGG	TTA	GGA	AAA	GAT	GCC	AAT	2015
Leu	Aşp		QTT	Glu	Gln	Ile	Phe	Ile	qrT	Ile	Gly	Lys	Asp	Ala	Asn	
		650					655					660				
GAA	GTT	GAG	AAA:	TCA	GAA	TCT	CIG	AAG	TCT	GCC	AAA	ATA	TAC	CTT	GAG	2063
Glu		Glu	Lys	Ser	Glu		Leu	Lys	Ser	Ala	Lys	Ile	Tyr	Leu	Glu	
	665					670					675					
ACC	GAC	CCT	TCT	GGA	AGA	GAC	AAG	AGG	ACG	CCA	TTA	GTC	ATC	ATA	AAA	2111
	Asp	Pro	Ser	Gly		Asp	Γλε	Arg	Thr		Ile	Val	Ile	Ile	Lys	
680					685					690					695	
CAG	GGT	CAT	GAG	CCA	CCT	ACT	TIC	ACA	GGC	TGG	TIC	CIG	œc	TGG	GAT	2159
				Pro											Asp	
				700					705					710		
TCC	AGC	AGG	TGG	TAAF	CIG	TT 1	TIGI	TAGG2	A A	AAAAC	DAAAI	ATP	ATG	SSC		2211
Ser	Ser	Arg														
			715													
AGCT	GICC	CA C	XXXX	GAAC	X AC	GAGO	TTGI	TT	ACTI	TAG	AAA	ATTA2	LCC I	CAGO	CATAT	2271
GGCI	TTTA	TT C	CCTC	CTIP	ea Da	TTGG	TTTG	AAA	TTTC	TTT	TAAI	CIG	r aa	TTTC	TTATG	2331
TTAA	TEAT.	TT I	ATAA	CTT	T CI	TATO	GACC	TAA :	ATE	ÆCT	CTGC	MGGZ	rig c	TGAC	CATATC	2391
TTTA	TATA	A DE	CTTI	TTA	A G		.G									2418

1.

SEQ ID NO:

Sequence length: 2630

Sequence Type: nucleic acid

Strandeness: double

5 Topology: linear

Molecule type: cDNA

Sequence characteristic:

Symbol Showing Characteristic: mat peptide

Location: 79. . 2223

5

10 Sequence description:

GAT	ATCA	CGC (GICO	cccs	GA G	CATO	GOGI	G CX	3GAG						IA TAC zu Tyr 5	96
														GTC Val		144
														CAC His		192
														AAG Lys		240
														GAG Glu		288
														ATG Met 85		336
														GGA Gly		384
GAG Glu	TCT Ser	AAT Asn 105	GAC Asp	TTT Phe	GTT Val	AGC Ser	TAT Tyr 110	TTC Phe	AAA Lys	GGC Gly	GGT Gly	CTG Leu 115	AAA Lys	TAC Tyr	AAG Lys	432
														GAC Asp		480
														AGA Arg		528
														TGC Cys		576

ATC	: ATI	r gac	CTI	, œc	: ACC	GAA	. ATT	TAT	, CYC	TOG	TGI	GTT	TCC	TCG	TGC	624
Ile	e Ile	e Asp	170		Thr	Glu	Ile	175		Trp	Cys	Gly	Ser 180		Cys	
AAC	: AAA	LAT	' GAA	. CGI	CIG	AAG	GCA	AAC	CAG	GTA	. GCT	ACT	GGC	ATT	æ	672
Asr	Lys	Tyr 185	Glu	Arg	Leu	Lys	Ala 190	Asn	Gln	Val	Ala	Thr 195	Gly	Ile	Arg	
m c																
TY	AAI AS	GAA Glu	<i>ىكى</i> د . ىىدد	AAA	. GGA Gly	AGG Am	TCT	GAA	CIA	ATT	GIC	GTG	GAA	GAA	GGA	720
	200)		27.2	ريي	205	541	Giu	Leu	116	210	vai	GIU	Glu	GΙΫ	
AGT	GAA	. ccc	TCA	GAA	CTT	ATA	AAG	GTC	ÆΤΥ	. egg	GAA	AAG	CCA	GAG	CTT	768
Ser	Glu	Pro	Ser	Glu	Leu	Ile	Lys	Val	Leu	Gly	Glu	Lys	Pro	Glu	Leu	
215					220					225					230	
		GGA														816
Pro	Asp	Gly	Gly		Asp	Asp	Asp	Ile		Ala	Asp	Ile	Ser	Asn	Arg	
. •				235					240					245		
AAA	ATG	CCT	AAA	CIA	TAC	ATG	GIT	TCA	GAT	GCA	AGT	GGC	TCC	ATG	AGA	864
Lys	Met	Ala		Leu	Tyr	Met	Val		Asp	Ala	Ser	Gly	Ser	Met	Arg	
			250			•		255					260			
GTG	ACT	GTG	gig	GCA	GAA	GAA	AAC	∞	TIC	TCA	ATG	GCA	ATG	CIG	CIG	912
Val	Thr	Val	Val	Ala	Glu	Glu	Asn	Pro	Phe	Ser	Met	Ala	Met	Leu	Leu	
		265					270					275				
TCT	GAA	GAA	TGC	TTT	ATT	TTG	GAC	CAC	œ	GCT	GCC	AAA	CAA	ATT	TTC	960
Ser	Glu	Glu	Cys	Phe	Ile	Leu	Asp	His	Gly	Ala	Ala	Lys	Gln	Ile	Phe	
	280					285					290					
GTA	TŒ	AAA	ŒT	AAA	GAT	GCT	AAT	α	CAA	GAG	AGG	AAG	GCT	GCA	ATG	1008
Val	Trp	Lys	Gly	ŗňz	Asp	Ala	Asn	Pro	Gln	Glu	Arg	Lys	Ala	Ala	Met	
295					300					305					310	
AAG	ACA	GCT	GAA	GAA	TTT	CIA	CAG	CAA	ATG	TAA	TAT	TCC	AAG	TAA	ACC	1056
Lys	Thr	Ala			Phe	Leu	Gln	Gln	Met	Asn	Tyr	Ser	Lys	Asn	Thr	
				315					320					325		
		CAA														1104
Gln	Ile	Gln		Leu	Pro	Glu			Glu	Thr	Pro	Ile	Phe	Lys	Gln	
			330					335					340			
TTT	TTT	AAG	GAC	TCG	AGA (GAT	AAA	GAT	CAG	AGT	GAT	GGC	TTC	œc	AAA	1152
Phe	Phe	Lys	Asp	Trp	Arg .	Asp	Lys	Asp	Gln	Ser	Asp	Gly	Phe	Gly	Lys	
		345					350					355				

											CAA					1200
Val	1yr 360		Thr	Glu	Lys	Val 365	Ala	Gln	Ile	Lys	Gln 370	Ile	Pro	Phe	ysp	
											GCC					1248
		Lys	Leu	His	Ser	Ser	Pro	Gln	Met	Ala	Ala	Gln	His	Asn	Met	
375					380				٠	385					390	
											CGT					1296
Val	Asp	Asp	Gly	Ser 395	Gly	Lys	Val	Glu	Ile 400	Trp	Arg	Val	Glu	Asn 405	Asn	
											GAA					1344
Gly	Arg	Ile	Gln 410	Val	Asp	Gln	Asn	Ser 415	Tyr	Gly	Glu	Phe	Tyr 420	Gly	Gly	
											GGA					1392
Asp	Cvs	Tyr 425	Ile	Ile	Leu	Tyr	Thr 430	Tyr	Pro	Arg	Gly	Gln 435	Ile	Ile	Tyr	
											CIG					1440
Thr	Trp 440	Gln	Gly	Ala	Asn	Ala 445	Thr	Arg	Asp	Glu	Leu 450	Thr	Thr	Ser	Ala	
TTC	CIG	ACT	GTT	CAG	TIG	GAT	ಾ	TCC	CTT	GGA	GGA	CAG	GCT	GIG	CAG	1488
	Leu	Thr	Val	Gln		Asp	Arg	Ser	Leu		Gly	Gln	Ala	Val	Gln	
455					460					465					470	
											CTA					1536
IIe	Arg	Val	Ser	Gln 475	Gly	ŢŇ2	Glu	Pro	Val 480	His	Leu	Leu	Ser	Leu 485	Phe	
											ACA					1584
Lys	Asp	Lys	Pro 490	Leu	Ile	Ile	Tyr	Lys 495	Asn	Gly	Thr	Ser	Lys 500	Lys	Gly	
											CAA					1632
Gly	Gln	Ala 505	Pro	Ala	Pro	Pro	Thr 510	Arg	Leu	Phe	Gln	Val 515	Arg	Arg	Asn	
											GTT					1680
	Ala 520	Ser	Ile	Thr	Arg	Ile 525	Val	Glu	Val	Asp	Val 530	Asp	Ala	Asn	Ser	
											CCA					1728
Leu 535	Asn	Ser	Asn	Asp	Val 540	Cys	Val	Leu	Lys	Leu 545	Pro	Gln	Asn	Ser	-	
					J4U					347					550	

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															GCA	1776
Tyr	Ile	Trp	Val	Gly 555		Gly	Ala	Ser	Gln 560	Glu	Glu	Glu	Lys	Gly 565	Ala	
GAG	TAI	GIA	. GCA	AGI	GIC	CIA	AAG	TGC	AAA	ACC	TIA	AGG	ATC	CAA	GAA	1824
														Gln		
GGC	GAG	GAG	CCA	GAG	GAG	TTC	TGG	AAT	TCC	CTT	GGA	œ	AAA	AAA	GAC	1872
Gly	Glu	. Glu 585		Glu	Glu	Phe	Trp	Asn	Ser	Ĺeu	Gly	Gly 595	Lys	Lys	Asp	
TAC	CAG	ACC	TCA	CCA	CIA	CIG	GAA	ACC	CAG	CT	GAA	GAC	CAT	CCA	CCT	1920
Tyr	Gln 600		Ser	Pro	Leu	Leu 605	Glu	Thr	Gln	Ala	Glu 610	Asp	His	Pro	Pro	
œ	CTT	TAC	GGC	TGC	TCT	AAC	AAA	ACT	GGA	AGA	TTT	GTT	ATT	GAA	GAG	1968
Arg 615	Leu	Tyr	Gly	Cys	Ser 620	Asn	Lys	Thr	Gly	Ar g 625	Phe	Val	Ile	Glu	Glu 630	
ATT	CCA	GGA	GAG	TIC	ACC	CAG	GAT	GAT	TTA	GCT	GAA	GAT	CAT	GTC	AŢG	2016
Ile	Pro	Gly	Glu	Phe 635	Thr	Gln	Asp	Asp	Leu 640	Ala	Glu	Asp	Asp	Val 645	Met	
														CAT		2064
Leu	Leu	yzb	Ala 650	Trp	Glu.	Gln	Ile	Phe 655	Ile	Trp	Ile	Gly	Lys 660	Asp	Ala	
														TAC		2112
Asn	Glu	Val 665	Glu	Lys	Lys	Glu	Ser 670	Leu	Lys	Ser	Ala	Lys 675	Met	Tyr	Leu	
GAG	ACA	GAC	CCT	TCT	GGA	AGA	GAC	AAG	AGG	ACA	CCA	ATT	GTC	ATC	ATA	2160
														Ile		
AAA																2208
L <u>v</u> s 695	Gln	Gly	His	Glu	Pro 700	Pro	Thr	Phe	Thr	Gly 705	ΩΥT	Phe	Leu	Gly	Trp 710	
GAT	TCC	AGC	AAG	TCG	TAAA	TTGG	TA T	TIGI	ΆΑΑΡ	A GC	`AAAC	'AAAC	: ATT	ACAA	.GGC	2263
Asp			ŗàz									-		- · - •	-	- ~ ~
AGTI	ATCI	CA I	TGCT	GTT	тс	GAGA	<i>G</i> GAA	. 000	GAAA	AGC	TITI	TGCI	TEA T	TIGI	CTTT	2323
GAAA	ATTA	AG G	CIG	GCGC	ىتى ئ	سکک	ראכא	۳,	ע מיניבו	т <u>т</u>	CDCC	יידי	, , , , , , , , , , , , , , , , , , , 	~~~	יאתייאר	2202

GTAGGCGGAT	CACTGGGGTC	AGGATTTCGA	GACCAGCCIG	GCCAACATGG	CGAAACCTCG	2443
CCTCTACTAA	AAATACAAAA	.AATTAGCTG	CCCTTCCTTCC	TGCACGCCTG	TAGTCCCTGC	2503
TACITOGAAG	GCTGAGACAG	GAAAATTGCT	TGAGCCCAGG	AGGCTGAGGT	TGCAGTGAGC	2563
CAGGATTGCG	CCACCACACT	CC*ECCIGGG	CAACAGAGAC	TCIGICICAA	AAAAAAAA	2623
AAAAAA						2630

SEQ ID NO: 6

Sequence length: 16

Sequence Type: amino acid

Topology: linear

5 Molecule type: peptide

Sequence description: LNHVLTNDLTAKRLLH

SEQ ID NO: 7

Sequence length: 16

10 Sequence Type: amino acid

Topology: linear

Molecule type: peptide

Sequence description: KVYVTEKVAQIKQIPF